



SEQUENCE LISTING

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Falkner, Falko-Guenter
Dorner, Friedrich
Baxter Aktiengesellschaft

<120> Factor IX/Factor IXa Activating Antibodies and Antibody Derivatives

<130> 20695C-005900US

<140> US 09/661,992
<141> 2000-09-14

<150> AT A157600
<151> 1999-09-14

<160> 112

<170> PatentIn Ver. 2.1

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oligonucleotide MOCMFOR

<400> 3
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line 193/AD3 heavy chain CDR3 region

<400> 5
Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr
1 5 10

<210> 6
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line 193/K2 heavy chain CDR3 region

<400> 6
Asp Gly Gly His Gly Tyr Gly Ser Ser Phe Asp Tyr
1 5 10

<210> 7
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line 193/AB2 (derived from antibody 198/B1) heavy
chain CDR3 region, peptide B1

<400> 7
Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val
1 5 10

<210> 8
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<223> Description of Artificial Sequence:hybridoma cell
line 198/A1 heavy chain CDR3 region, peptide A1

<400> 8
Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val
1 5 10

<210> 9
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derived mutated peptide A1/1 scrambled versioon of
A1

<400> 10
Val Tyr Gly Phe Gly Trp Gly Tyr Glu Val Asn Asp Tyr
1 5 10

<210> 11
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derived mutated peptide A1/2

<400> 11
Glu Glu Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Glu
1 5 10 15

Glu Glu

<210> 12
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derived mutated peptide A1/3

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Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 13
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derived mutated peptide A1/4 scrambled version of
A1/2

<400> 13
Glu Tyr Gly Glu Gly Tyr Gly Glu Val Asn Glu Tyr Asp Glu Phe Glu
1 5 10 15

Trp Glu

<210> 14
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derived mutated peptide A1/5 scrambled version of
A1/3

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Val Arg Tyr Arg Asn Arg Tyr Arg Trp Gly Tyr Arg Gly Arg Phe Gly
1 5 10 15

Asp Glu

<210> 15
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derived mutated peptide A1/3-scr3 scrambled
version of A1/3

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1 5 10 15

Arg Arg

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<210> 19
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derived mutant peptide A1/3-13 Alanine scan
E-1-A-1

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1 5 10 15

Arg Arg

<210> 20
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derived mutant peptide A1/3-1 Alanine scan G-2-A-2

<400> 20
Arg Arg Arg Glu Ala Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 21
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derived mutant peptide A1/3-2 Alanine scan G-3-A-3

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1 5 10 15

Arg Arg

<210> 22
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derived mutant peptide A1/3-3 Alanine scan G-4-A-4

<400> 22
Arg Arg Arg Glu Gly Gly Ala Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 23
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derived mutant peptide A1/3-4 Alanine scan Y-5-A-5

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Arg Arg Arg Glu Gly Gly Ala Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 24
<211> 18
<212> PRT
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<220>
<223> Description of Artificial Sequence:antibody 198/A1
derived mutant peptide A1/3-5 Alanine scan Y-6-A-6

<400> 24
Arg Arg Arg Glu Gly Gly Tyr Ala Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 25
<211> 18
<212> PRT
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<220>
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derived mutant peptide A1/3-6 Alanine scan V-7-A-7

<400> 25
Arg Arg Arg Glu Gly Gly Tyr Tyr Ala Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 26
<211> 18
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derived mutant peptide A1/3-7 Alanine scan N-8-A-8

<400> 26
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Ala Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 27
<211> 18
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derived mutant peptide A1/3-8 Alanine scan W-9-A-9

<400> 27
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Ala Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 28
<211> 18
<212> PRT
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<220>
<223> Description of Artificial Sequence:antibody 198/A1
derived mutant peptide A1/3-9 Alanine scan
Y-10-A-10

<400> 28
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Ala Phe Asp Arg
1 5 10 15

Arg Arg

<210> 29
<211> 18
<212> PRT
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derived mutant peptide A1/3-10 Alanine scan
F-11-A-11

<400> 29
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Ala Asp Arg
1 5 10 15

Arg Arg

<210> 30
<211> 18
<212> PRT
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derived mutant peptide A1/3-11 Alanine scan
D-12-A-12

<400> 30
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Ala Arg
1 5 10 15

Arg Arg

<210> 31
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derived mutant peptide A1/3-12srmb scrambled
version

<400> 31
Arg Arg Arg Tyr Val Tyr Asn Gly Trp Gly Tyr Phe Glu Gly Ala Arg
1 5 10 15

Arg Arg

<210> 32
<211> 18
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derived mutant peptide A1/3-22 Glutamic acid scan
G-2-E-2

<400> 32
Arg Arg Arg Glu Glu Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 33
<211> 18
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derived mutant peptide A1/3-23 Glutamic acid scan
G-3-E-3

<400> 33
Arg Arg Arg Glu Gly Glu Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 34
<211> 18
<212> PRT
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derived mutant peptide A1/3-24 Glutamic acid scan
G-4-E-4

<400> 34
Arg Arg Arg Glu Gly Glu Glu Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 35
<211> 18
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<220>
<223> Description of Artificial Sequence:antibody 198/A1
derived mutant peptide A1/3-26 Glutamic acid scan
Y-5-E-5

<400> 35
Arg Arg Arg Glu Gly Glu Glu Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 36
<211> 18
<212> PRT
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<223> Description of Artificial Sequence:antibody 198/A1
derived mutant peptide A1/3-27 Glutamic acid scan
Y-6-E-6

<400> 36
Arg Arg Arg Glu Gly Gly Tyr Glu Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 37
<211> 18
<212> PRT
<213> Artificial Sequence

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derived mutant peptide A1/3-28 Glutamic acid scan
V-7-E-7

<400> 37
Arg Arg Arg Glu Gly Gly Tyr Tyr Glu Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 38
<211> 18
<212> PRT
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derived mutant peptide A1/3-29 Glutamic acid scan
N-8-E-8

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Arg Arg Arg Glu Gly Gly Tyr Tyr Val Glu Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 39
<211> 18
<212> PRT
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<220>
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derived mutant peptide A1/3-30 Glutamic acid scan
W-9-E-9

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1 5 10 15

Arg Arg

<210> 40
<211> 18
<212> PRT
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derived mutant peptide A1/3-31 Glutamic acid scan
Y-10-E-10

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1 5 10 15

Arg Arg

<210> 41
<211> 18
<212> PRT
<213> Artificial Sequence

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derived mutant peptide A1/3-32 Glutamic acid scan
F-11-E-11

<400> 41
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Glu Asp Arg
1 5 10 15

Arg Arg

<210> 42
<211> 18
<212> PRT
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derived mutant peptide A1/3-33 Glutamic acid scan
D12-E-12

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1 5 10 15

Arg Arg

<210> 43
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derived mutant peptide A1/3-34srmb scrambled
version

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1 5 10 15

Arg Arg

<210> 44
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<210> 45
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derived mutated peptide B1/4

<400> 45
Arg Glu Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Arg
1 5 10

<210> 46
<211> 14
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derived mutated peptide B1/5 scrambled version

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Phe Gly Val Gly Tyr Arg Gly Glu Thr Arg Asn Phe Asp Trp
1 5 10

<210> 47
<211> 18
<212> PRT
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<220>
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derived mutated peptide B1/6

<400> 47
Glu Glu Glu Glu Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Glu
1 5 10 15

Glu Glu

<210> 48
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:antibody 198/B1
derived mutated peptide B1/7

<400> 48
Arg Arg Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 49
<211> 18
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derived mutated peptide B1/7scr3 scrambled version

<400> 49
Arg Arg Arg Phe Gly Val Gly Tyr Gly Glu Thr Asn Phe Asp Trp Arg
1 5 10 15

Arg Arg

<210> 50
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mouse V-H back
primer VH1BACK-SfiI

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<210> 51
<211> 56
<212> DNA
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<223> Description of Artificial Sequence:mouse V-H back
primer VH1BACKSfi

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<210> 52
<211> 56
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:mouse V-H back
primer VH2BACKSfi

<400> 52
gtcctcgcaa ctgcggccca gccggccatg gccgatgtgc agttcagga gtcrgg 56

<210> 53
<211> 56
<212> DNA
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<223> Description of Artificial Sequence:mouse V-H back primer VH3BACKSfi

<400> 53
gtcctcgcaa ctgcggccca gccggccatg gcccaggtgc agctgaagsa gtcagg 56

<210> 54
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<210> 55
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<210> 56
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<210> 57
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primer VH8BACKSfi

<400> 57
gtcctcgcaa ctgcggccca gccggccatg gccgagggttc agttcagca gtctgg 56

<210> 58
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<223> Description of Artificial Sequence:mouse V-H back
primer VH10BACKSfi

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<210> 59
<211> 56
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primer VH11BACKSfi

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<210> 60
<211> 68
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<223> Description of Artificial Sequence:mouse J-H
forward primer VH1FOR2LiAsc

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ttggccccc 68

<210> 61
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mouse J-H
forward primer JH1FORLiAsc

<400> 61
accgccagag ggcgcgcac ctgaaccgcc tccacctgag gagacgggtga ccgtggccc 60

<210> 62
<211> 60
<212> DNA
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<223> Description of Artificial Sequence:mouse J-H
forward primer JH2FORLiAsc

<400> 62
accgccagag gcgcgccccac ctgaaccgcc tccacctgag gagactgtga gagtggtgcc 60

<210> 63
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forward primer JH3FORLiAsc

<400> 63
accgccagag gcgcgccccac ctgaaccgcc tccacctgca gagacagtga ccagagtc 60

<210> 64
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<213> Artificial Sequence

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forward primer JH4FORLiAsc

<400> 64
accgccagag gcgcgccccac ctgaaccgcc tccacctgag gagacggtga ctgaggttcc 60

<210> 65
<211> 60
<212> DNA
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back primer VK2BACK-LiAscI

<400> 65
ggttcagatg ggcgcgcctc tggcggtggc ggatcgacat ttgagctcac ccagtctcca 60

<210> 66
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<220>
<223> Description of Artificial Sequence:mouse V-kappa
back primer VK1BACKLi Asc

<400> 66
ggttcagatg ggccgcgcctc tggcggtggc ggatcggaca ttgtgatgwc acagtctcc 59

<210> 67
<211> 59
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back primer VK2BACKLi Asc

<400> 67
ggttcagatg ggccgcgcctc tggcggtggc ggatcggatg ttktgatgac ccaaactcc 59

<210> 68
<211> 59
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back primer VK3BACKLi Asc

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<210> 69
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<223> Description of Artificial Sequence:mouse V-kappa
back primer VK4BACKLi Asc

<400> 69
ggttcagatg ggccgcgcctc tggcggtggc ggatcggaca ttgtgctgac mcartctcc 59

<210> 70
<211> 59
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<223> Description of Artificial Sequence:mouse V-kappa
back primer VK5BACKLi Asc

<400> 70
ggttcagatg ggccgcgcctc tggcggtggc ggatcgsaaa wtgtkctcac ccagtctcc 59

<210> 71
<211> 59
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:mouse V-kappa
back primer VK6BACKLi Asc

<400> 71
ggttcagatg ggccgcgc ctc tggcggtggc ggatcgaya tyvwgatgac mcagwctcc 59

<210> 72
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mouse V-kappa
back primer VK7BACKLi Asc

<400> 72
ggttcagatg ggccgcgc ctc tggcggtggc ggatcgaaa ttgttctcac ccagtctcc 59

<210> 73
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mouse V-kappa
back primer VK8BACKLi Asc

<400> 73
ggttcagatg ggccgcgc ctc tggcggtggc ggatcgcat tattgcaggt gcttgtggg 59

<210> 74
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mouse J-kappa
forward primer JK1NOT10

<400> 74
gagtcattct gcggccgccc gttt gatttc cagttggtg cc 42

<210> 75
<211> 42
<212> DNA
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<220>
<223> Description of Artificial Sequence:mouse J-kappa
forward primer JK2NOT10

<400> 75
gagtcattct gcggccgccc gttt gatttc cagttggtc cc 42

<210> 76
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
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forward primer JK3NOT10

<400> 76
gagtcattct gcggccgccc gttttatttc cagtctggtc cc 42

<210> 77
<211> 42
<212> DNA
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<220>
<223> Description of Artificial Sequence:mouse J-kappa
forward primer JK4NOT10

<400> 77
gagtcattct gcggccgccc gttttatttc caactttgtc cc 42

<210> 78
<211> 42
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:mouse J-kappa
forward primer JK5NOT10

<400> 78
gagtcattct gcggccgccc gtttcagctc cagcttggtc cc 42

<210> 79
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mychis6-co

<400> 79
ggccgcagaa caaaaactca tctcagaaga ggatctgaat ggggccccac atcaccatca 60
ccatcaactaa taag 74

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<223> Description of Artificial Sequence:oligonucleotide
mycchis-ic

<400> 80
 aattcttatt agtgatggtg atggtgatgt gccggccat tcagatcctc ttctgagatg 60
 agtttttgtt ctgc 74

<210> 81
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 <223> Description of Artificial Sequence:scFv from
 hybridoma cell line 193/AD3

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 gaggtgaagc tggggagtc tggacctgag ctgaagaagc ctggagagac agtcaagatc 60
 tcctgcaagg cttctggta tatcttcaca aactatggaa tgaactgggt gaagcaggct 120
 ccagggaaagg gtttaaagtg gatgggctgg ataaacacct acactggaga gccaacatata 180
 gctgatgact tcaagggacg gtttgccttc tcttggaaa cctctgccag cactgcctat 240
 ttgcagatca acaacctcaa aaatgaggac acggctacat atttctgtgc attatatgg 300
 aactccccca aggggtttgc ttactggggc caagggactc tggtcactgt ctctgcaggt 360
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 cagagtgtga gtaatgatgt agcttggtac caacagaagc cggggcagtc tcctaaacta 540
 ctgatgtact atgcattccaa tcgctacact ggagtccctg atcgcttcac tggcagtgaa 600
 tatgggacgg atttcacttt caccatcagc actgtgcagg ctgaagacct ggcagtttat 660
 ttctgtcagc aggattatgg ctctcctccc acgttcggag ggggcaccaa gctggaaatt 720
 aaacgg 726

<210> 82
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 hybridoma cell line 193/AD3

<400> 82
 Glu Val Lys Leu Val Glu Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asn Tyr
 20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
 50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
 85 90 95

Ala Leu Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Arg Ala
115 120 125

Ser Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Lys Phe
 130 135 140

Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
145 150 155 160

Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 165 170 175

Ser Pro Lys Leu Leu Met Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val
 180 185 190

Pro Asp Arg Phe Thr Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr
 195 200 205

Ile Ser Thr Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln
210 215 220

Asp Tyr Gly Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lvs Arg

```
<210> 83
<211> 747
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence:scFv from
hybridoma cell line 193/K2

<400> 83	gaagtgcagc	tggggagtc	tggggaggc	ctagtgaagc	ctggagggtc	cctgaaactc	60
	tcctgtcag	cctctggatt	cactttcagt	acctatacca	tgtctgggt	tcgcccagact	120
	ccggagaaga	ggctggagtg	ggtcgcaacc	attagtagtg	gtggtagtta	cacctactat	180
	ccagacagtg	tgagggcccg	attcaccatc	tccagagaca	atgccaagaa	caccctgtac	240
	ctgcaaatga	gcagtctgaa	gtctgaggac	acagccatgt	attactgtac	aagagatggg	300
	ggacacgggt	acggtagtag	cttgcgtac	tggggccaag	gcaccactct	cacagtctcc	360
	tcaggtggag	gccccgtcagg	tgggcgcgccc	tctggcggtg	gcggatcgca	aattgtgtct	420
	acccagtc	caactccct	gcctgtcagt	cttggagatc	aagctccat	ctttgtcaga	480
	tctagtcaga	gcattgtaca	tagtaatgga	aacacctatt	tagaatggta	cctgcagaaa	540
	ccaggccagt	ctccaaagct	cctgatctac	aaagtttcca	accgattttc	tggggtccca	600
	gacaaattca	gtggcagtgg	atcagggaca	gatttcacac	tcaagatcg	cagagtggag	660
	gctgaggatc	tgggagttt	ttactgttt	caaggttcac	atgttccgtg	gacgttccgt	720
	ggaggcacca	agctggaaat	caaacgg				747

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<210> 84
<211> 249
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:scFv from
hybridoma cell line 193/K2

<400> 84
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15
 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
 20 25 30
 Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
 35 40 45
 Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val
 50 55 60
 Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Thr Arg Asp Gly Gly His Gly Tyr Gly Ser Ser Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
 115 120 125
 Arg Ala Ser Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro
 130 135 140
 Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg
 145 150 155 160
 Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp
 165 170 175
 Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
 180 185 190
 Ser Asn Arg Phe Ser Gly Val Pro Asp Lys Phe Ser Gly Ser
 195 200 205
 Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
 210 215 220
 Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly
 225 230 235 240
 Gly Gly Thr Lys Leu Glu Ile Lys Arg
 245

<210> 85
 <211> 747
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:scFv from
 hybridoma cell line 198/AB2 (subclone of 198/B1)

<400> 85
 gaggtgcagc ttcaggagtc agggggaggc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtcag cctctggatt cactttcagt agctatacca tgtcttgggt tcgccagact 120
 ccggagaaga ggctggagtg ggtcgcaacc attagtagtg gtggtagttc cacctactat 180
 ccagacagtg tgaagggccg attcaccatc tccagagaca atgccaagaa caccctgtac 240
 ctgcaaatga gcagtctgag gtctgaggac acagccatgt attactgtac aagagagggg 300
 gttggttca ccgtaactg gtacttcgtat gtctggggcg cagggactct ggtcaactgtc 360
 tctgcaggtg gaggcgggtc aggtgggcgc gcctctggcg gtggcggatc ggaaaatgtg 420
 ctcacccagt ctccagcttc tttggctgtg tctctagggc agagggccac catatcctgc 480
 agagccagtg aaagtgttga tagttatggc tataattttt tgcaactggta tcagcagata 540
 ccaggacagc cacccaaact cctcatctat cgtcatcca acctagagtc tgggatccct 600
 gccaggttca gtggcagtgg gtctaggaca gacttcaccc tcaccattaa tcctgtggag 660
 gctgatgtg ttgcaaccta ttactgtcag caaagtaatg aggatccgct cacgttcgg 720
 actgggacca gactggaaat aaaacgg 747

<210> 86

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:scFv from
hybridoma cell line 198/AB2 (subclone of 198/B1)

<400> 86

Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
 35 40 45

Ala Thr Ile Ser Ser Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Thr Arg Glu Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val Trp
 100 105 110

Gly Ala Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Ser Gly
 115 120 125

Gly Arg Ala Ser Gly Gly Ser Glu Asn Val Leu Thr Gln Ser
 130 135 140

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
 145 150 155 160

Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Tyr Asn Phe Met His Trp
 165 170 175

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala
 180 185 190

Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
 195 200 205
 Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val
 210 215 220
 Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly
 225 230 235 240
 Thr Gly Thr Arg Leu Glu Ile Lys Arg
 245

<210> 87
 <211> 747
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:scFv derived
 from hybridoma cell line 198/A1

<220>
 <221> modified_base
 <222> (1)..(747)
 <223> n = g, a, c or t

<400> 87
 gaggtgcagc ttcaggagtc agggggaggc ttagtgaagc ctggagggtc cctgaaaactc 60
 tcctgtgcag cctctggatt catttttagt agtatacca tgtctgggt tcgccagact 120
 ccggagaaga ggctggagtg ggtcgcaacc attagtagtg gtggtagttc cacctactat 180
 ccagacagtg tgaagggccg attcaccatc tccagagaca atgccaagaa caccctgtac 240
 ctgcaaatga gcagtctgaa gtctgaggac acagccatgt atcaactgtac aagagagggg 300
 ggtggttatt acgtcaactg gtacttcgat gtctgggcgc cagggcaccac ttcacagtc 360
 tcctcagggtg gaggcggtc aggtgggcgc gcctctggcg gtggcgatc ggacatttag 420
 ctcacncagt ctccagcttc tttggctgtg tctctaggc agagggccac catatcctgc 480
 agagccagtg aaagtgttga tagttatggc aagagttta tgcactggta ccagcagaaa 540
 ccagggcagc cacccaaact cctcatctt cgtgcattca acctagaatc tgggatccct 600
 gccaggttca gtggcagtgg gtctaggaca gacttcaccc tcaccattaa tcctgtggag 660
 gctgtatgtt ttgcnaccta ttactgtcag caaagtaatg aggtatccc cacgttcggg 720
 gctggacca gactggaaat aaaacgg 747

<210> 88
 <211> 249
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:scFv derived
 from hybridoma cell line 198/A1

<400> 88
 Glu Val Gln Leu Gln Glu Ser Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
 20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
 35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr His Cys
 85 90 95
 Thr Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val Trp
 100 105 110
 Gly Ala Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Ser Gly
 115 120 125
 Gly Arg Ala Ser Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser
 130 135 140
 Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
 145 150 155 160
 Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Lys Ser Phe Met His Trp
 165 170 175
 Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala
 180 185 190
 Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
 195 200 205
 Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val
 210 215 220
 Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly
 225 230 235 240
 Ala Gly Thr Arg Leu Glu Ile Lys Arg
 245

<210> 89
 <211> 2199
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:198A2
 scFv-alkaline phosphatase fusion protein (ORF of
 expression vector pDAP2-198AB2#100)

<220>
 <221> modified_base
 <222> (228)
 <223> n = g, a, c or t

<400> 89
 atgaaataacc tattgcctac ggcagccgct ggattgttat tactcgccgc ccagccggcc 60
 atggcggagg tgaagctggg ggagtctggg ggaggcttag tgaagcctgg agggtccctg 120
 aaactctctt gtgcagccctc tggattcaact ttcagtagct ataccatgtc ttgggttcgc 180
 cagactccgg agaagaggct ggagtgggtc gcaaccatta gtatgtggngg tagttccacc 240
 tactatccag acagtgtgaa gggccgatcc accatctcca gagacaatgc caagaacacc 300

ctgtacctgc aaatgagcag tctgaggctc gaggacacag ccatgtatta ctgtacaaga 360
 gagggggggtg gtttaccgt caactggta tcgtatgtct gggcgccagg aacctcagtc 420
 accgtctcct caggggagg cggttcaggt gggcgccct ctggcggtgg cggatcgac 480
 attgtgctga cacagtctcc agttcttgc gctgtgtctc tagggcagag ggccaccata 540
 tcctgcagag ccagtgaag tggatagt tatggctata atttatgca ctggtatcag 600
 cagataccag gacagccacc caaactcctc atctatcgta catccaaacct agagtctggg 660
 atccctgcca gttcagtgg cagtgggtct aggacagact tcaccctcac cattaatcct 720
 gtggaggctg atgatgttgc aaccttatac tgcagcaaa gtaatgagga tccgctca 780
 ttcggtactg ggaccagact gaaaataaaa cggcgccg cagcccgacc accagaaatg 840
 cctgttctgg aaaaccggc tgctcaggc gatattactg caccggccg tgctcgccgt 900
 ttaacgggtg atcagactgc cgctctgcgt gattctctta gcgataaaacc tgcaaaaaat 960
 attatgtc tgattggcga tggatggg gactcggaaa ttactgccgc acgtaattat 1020
 gccgaagggtg cggcgccct tttaaaggt atagatgcct taccgcttac cgggcaatac 1080
 actcaactatg cgctgaataa aaaaaccggc aaaccggact acgtcaccga ctcggctgca 1140
 tcagcaaccg cctggtaac cggtgtcaaa acctataacg gcgctggg cgtcgatatt 1200
 cacaaaaaag atcaccac gattctgaa atggcaaaag cccgaggtct ggcgaccgg 1260
 aacgttctta cccgaggtt gcaggatgcc acgccccgtg cgctgggtgc acatgtgacc 1320
 tcgcgcaaat gctacggtcc gagcgcgacc agtaaaaat gtccggtaa cgctctggaa 1380
 aaaggcggaa aaggatcgat taccgaacag ctgcattaaacg ctgcgtccga cgttacgctt 1440
 ggcggccggc caaaaacctt tgctgaaacg gcaaccgtg gtgaatggca gggaaaaacg 1500
 ctgcgtgaac aggacacaggc gcgtggttat cagttggtaa gcatgtgc ctcactgaat 1560
 tcggtgacgg aagcgaatca gcaaaaaccc ctgctggcc tgtttgcgat cggcaatatg 1620
 ccagtgcgt ggctaggacc gaaagcaacg taccatggca atatcgataa gcccgcagtc 1680
 acctgtacgc caaatccgca acgtaatgac agtgtaccaa ccctggcgca gatgaccgac 1740
 aaagccattg aattgtttag taaaaatgaa aaaggcttt tcctgcagaat tgaagggtgc 1800
 tcaatcgata aacaggatca tgctgcgaat cctgtggc aattggcga gacggctcgat 1860
 ctgcgtgaag ccgtacaacg ggcgttgaa ttgcataaaa aggagggtaa cacgctggc 1920
 atagtcaccc ctgatcacgc ccacgcccagc cagattgttg cgccggatac caaagctccg 1980
 ggcctcaccc aggccctaaa taccaaagat ggcgcagtga tggtgatgag ttacggaaac 2040
 tccgaagagg attcacaaga acataccggc agtcagttgc gtattggcgt gatggcccg 2100
 catccgcaca atgttggcgttgg actgaccgac cagaccgatc tcttctacac catgaaagcc 2160
 gctctggggg atatcgacca ccatcaccat caccattaa 2199

<210> 90
 <211> 732
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:198A2
 scFv-alkaline phosphatase fusion protein (ORF of
 expression vector pDAP2-198AB2#100)

<400> 90
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15
 Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly
 20 25 30
 Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
 35 40 45
 Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu
 50 55 60
 Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr
 65 70 75 80

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
 85 90 95
 Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp
 100 105 110
 Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Phe Thr Val Asn
 115 120 125
 Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser
 130 135 140
 Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Asp
 145 150 155 160
 Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
 165 170 175
 Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly
 180 185 190
 Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
 195 200 205
 Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg
 210 215 220
 Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro
 225 230 235 240
 Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu
 245 250 255
 Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala
 260 265 270
 Ala Ala Ala Arg Ala Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala
 275 280 285
 Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp
 290 295 300
 Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn
 305 310 315 320
 Ile Ile Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala
 325 330 335
 Ala Arg Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp
 340 345 350
 Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys
 355 360 365
 Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala
 370 375 380
 Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile
 385 390 395 400

His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly
 405 410 415
 Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro
 420 425 430
 Ala Ala Leu Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser
 435 440 445
 Ala Thr Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys
 450 455 460
 Gly Ser Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu
 465 470 475 480
 Gly Gly Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp
 485 490 495
 Gln Gly Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu
 500 505 510
 Val Ser Asp Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln
 515 520 525
 Lys Pro Leu Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp
 530 535 540
 Leu Gly Pro Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val
 545 550 555 560
 Thr Cys Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala
 565 570 575
 Gln Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly
 580 585 590
 Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala
 595 600 605
 Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala
 610 615 620
 Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val
 625 630 635 640
 Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp
 645 650 655
 Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala
 660 665 670
 Val Met Val Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Glu His
 675 680 685
 Thr Gly Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn
 690 695 700
 Val Val Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala
 705 710 715 720

Ala Leu Gly Asp Ile Ala His His His His His His
 725 730

<210> 91
 <211> 978
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:plasmid
 pZip-198AB2#102

 <220>
 <221> modified_base
 <222> (1)...(978)
 <223> n = g, a, c or t

 <400> 91
 atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgccgc ccagccggcc 60
 atggcggagg tgaagctggg ggagtctggg ggaggccttag tgaagcctgg agggtcctcg 120
 aaactctcct gtgcagccct tggattcaact ttcagtagct ataccatgtc ttgggttcgc 180
 cagactccgg agaagaggct ggagtgggtc gcaaccattt aatgtgggg tagttccacc 240
 tactatccag acagtgtgaa gggccgattt accatctcca gagacaatgc caagaacacc 300
 ctgtacctgc aaatgagcag tctgaggtct gaggacacag ccatgttata ctgtacaaga 360
 gaggggggggtg gtttaccgtt caactgggtc ttcatgtct ggggcgcagg aacctcagtc 420
 accgtctcct cagggtggagg cgggttcaggt gggcgcgcct ctggcgttgg cggatcggac 480
 atttgtctgaa cacagtntcc agcttcttg gctgtgtctc tagggcagag ggccaccata 540
 tcntgcagag ccagtgaaag tggatgtat tattgtata attttatgca ctggtatcag 600
 cagataccag gacagccacc caaactcctc atctatcgtt catccaacct agagtctggg 660
 atccctgcctt ggttcaagtgg cagtggttctt aggacagact tcaccctcac cattaaatcct 720
 gtggaggctg atgatgttgc aacattttac tgcgttgc gtaatgagga tccgctcagc 780
 ttccgttactg ggaccagact gggaaataaaa cgggcggcccg caccgaagcc ttccactccg 840
 cccgggtttt cccgtatgaa acagctgaa gacaaatgtt agggacttct tagcaagaac 900
 taccatcttag aaaaacgaggt agctcgatctt aaaaatgtt ttggtaacg tggtggtcac 960
 catcaccatc accattaa 978

<210> 92
 <211> 325
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:plasmid
 pZip-198AB2#102

 <220>
 <221> MOD_RES
 <222> (166)
 <223> Xaa = Cys, Tyr, Ser or Phe

 <400> 92
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15

 Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly
 20 25 30

 Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
 35 40 45

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu
 50 55 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr
 65 70 75 80

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
 85 90 95

Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp
 100 105 110

Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Phe Thr Val Asn
 115 120 125

Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser
 130 135 140

Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Asp
 145 150 155 160

Ile Val Leu Thr Gln Xaa Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
 165 170 175

Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly
 180 185 190

Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
 195 200 205

Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg
 210 215 220

Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro
 225 230 235 240

Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu
 245 250 255

Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala
 260 265 270

Ala Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln
 275 280 285

Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu
 290 295 300

Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His
 305 310 315 320

His His His His
 325

<210> 93
 <211> 2190
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mAB#8860
 scFv-alkaline phosphatase fusion protein (vector
 construct pDAP2-8860scFv#11)

<400> 93

atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgccgc ccagccggcc 60
 atggccgagg ttcaagcttca gcagtctgga cctgagctgg tgaagcccg ggcctcagtg 120
 aagatttcct gcaaagcttc tggctacgca ttcaagtagct cttggatgaa ctgggtgaag 180
 cagaggcctg gacagggtct tgagtggatt ggacggattt atcctggaaa tggagatact 240
 aactacaatg ggaagttcaa gggcaaggcc acactgactg cagacaatac ctccagcaca 300
 gcctacatgc agctcagcag cctgaccctt gtggactctg cggcttattt ctgtgcagat 360
 gttaacgtat attactatgc tatggactac tgggtcaag gaacctcagt caccgtctcc 420
 tcaggtggag gcggttcagg tgggcgcgc tctggcggtg gcgatcgca aattgttctc 480
 acccagtctc ctgcttcctt agctgtatct ctggggcaga gggccaccat ctcatgcagg 540
 gccagcaaaa gtgtcagtagt atctggctat agttagatgc actggtagcca acagaaacca 600
 ggacagccac ccaaactcct catctatctt gcatccaacc tagaatctgg ggtccctgccc 660
 aggttcagtg gcagtgggtc tgggacagac ttcaaccctca acatccatcc tgggaggag 720
 gaggatgctg caacctatta ctgtcagcac agtagggagc ttccctcgac gttcggtgga 780
 ggcaccaagc tggaaatcaa acgggcggcc gcagccccggg caccagaaat gcctgttctg 840
 gaaaaccggg ctgctcaggg cgatattact gcacccggcg gtgctcggc ttaacgggt 900
 gatcagactg ccgctctgctg tgattctt agcgataaac ctgcaaaaaa tattatttt 960
 ctgattggcg atggatggg ggactcgaa attactgccc cacgttaatta tgccgaaggt 1020
 gcgccggct tttttaagg tatagatgcc ttaccgccta ccggcaata cactcactat 1080
 gcgctgaata aaaaaaccgg caaaccggac tacgtcaccg actcggctgc atcagcaacc 1140
 gcctggtcaa ccgggtcaaa aacctataac ggccgcgtgg gcgtcgatat tcacgaaaaa 1200
 gatcaccctaa cgattctgga aatggaaaaa gcccggcgtc tggcaccgg taacgtttct 1260
 acccgagagt tgcaaggatgc cacgcccgcgc gcgtcggtgg cacatgtgac ctgcgcacaa 1320
 tgctacggc cgagcgcgc acgtaaaaa tgccgggtt acgctctgga aaaaggcgg 1380
 aaaggatcga ttaccgaaca gctgcttaac gctcggtccgc acgttacgct tggccggc 1440
 gcaaaaaact ttgctgaaac ggcaaccgcgt ggtgaatggc agggaaaaac gtcgtgaa 1500
 caggcacagg cgctggta tcagttgtg agcgatgctg cctcactgaa ttcggtgacg 1560
 gaagcgaatc agaaaaacc cctgcttggc ctgtttgtg acggcaatat gccagtgcgc 1620
 tggctaggac cgaaagcaac gtaccatggc aatatcgata agccgcgtt caccgttacg 1680
 ccaaattccgc aacgtaatga cagtgtacca accctggcgc agatgaccga caaagccatt 1740
 gaattgttga gtaaaaaatga gaaaggctt ttccctgcaag ttgaagggtc gtcattcgat 1800
 aaacaggatc atgctgcgaa tccttgggg caaattggcg agacggtcgat ttcgtatgaa 1860
 gccgtacaac gggcgctgga attcgctaaa aaggagggtt acacgctgtt catagtcacc 1920
 gctgatcactc cccacgcgc ctagattgtt gcggccggata ccaaagctcc gggcctcacc 1980
 caggcgctaa ataccaaaga tggcgcgtt atggatgatga gttacggaa ctccgaagag 2040
 gattcacaag aacataccgg cagtcagttt cgtattgcgg cgtatggccc gcatgccgc 2100
 aatgttggtg gactgaccga ccagaccgt ctcttctaca ccatgaaagc cgctctgggg 2160
 gatatgcac accatcacca tcaccattaa 2190

<210> 94

<211> 729

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mAB#8860
 scFv-alkaline phosphatase fusion protein (vector
 construct pDAP2-8860scFv#11)

<400> 94

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
 20 25 30

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
 35 40 45

Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
 50 55 60

Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
 65 70 75 80

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
 85 90 95

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp
 100 105 110

Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met
 115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Gln Ile Val Leu
 145 150 155 160

Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr
 165 170 175

Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 180 185 190

Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 195 200 205

Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
 210 215 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu
 225 230 235 240

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg
 245 250 255

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ala
 260 265 270

Arg Ala Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala Gln Gly Asp
 275 280 285

Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala
 290 295 300

Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile Leu
 305 310 315 320

Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn
 325 330 335

Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro
 340 345 350

Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys Thr Gly Lys
 355 360 365
 Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser Thr
 370 375 380
 Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile His Glu Lys
 385 390 395 400
 Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr
 405 410 415
 Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu
 420 425 430
 Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser
 435 440 445
 Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile
 450 455 460
 Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly
 465 470 475 480
 Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys
 485 490 495
 Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp
 500 505 510
 Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu
 515 520 525
 Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro
 530 535 540
 Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr
 545 550 555 560
 Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr
 565 570 575
 Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe Leu
 580 585 590
 Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala Ala Asn Pro
 595 600 605
 Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala Val Gln Arg
 610 615 620
 Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val Ile Val Thr
 625 630 635 640
 Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala
 645 650 655
 Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala Val Met Val
 660 665 670

Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Glu His Thr Gly Ser
 675 680 685
 Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly
 690 695 700
 Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly
 705 710 715 720
 Asp Ile Ala His His His His His His
 725

<210> 95
 <211> 969
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mAB #8860
 scFv-leucine zipper fusion protein (miniantibody
 vector construct p8860-Zip#1.2)

<400> 95
 atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgccgc ccagccggcc 60
 atggcggagg ttcagcttca gcagtcttga cctgagctgg tgaagcccg ggcctcagtg 120
 aagatttcct gcaaagcttc tggctacgca ttcaagtagct cttggatgaa ctgggtgaag 180
 cagaggcctg gacagggct tgagtggatt ggacggattt atcctggaaa tggagatact 240
 aactacaatg ggaagttcaa gggcaaggcc acactgactg cagacaaatc ctccagcaca 300
 gcctacatgc agctcagcag cctgacctct gtggactctg cggcttattt ctgtgcagat 360
 gttaacgtat attactatgc tatggactac tgggtcaag gaacctcagt caccgtctcc 420
 tcaggtggag gcgggtcagg tgggcgcgcc tctggcggtg gcggatcgca aattgttctc 480
 acccagtctc ctgcttcctt agctgtatct ctggggcaga gggccaccat ctcatgcagg 540
 gccagcaaaa gtgtcagtagc atctggctat agttatatgc actggtagcca acagaaacca 600
 ggacagccac ccaaactctt catctatctt gcatccaacc tagaatctgg ggtccctgcc 660
 aggttcagtg gcagtggtc tgggacagac ttacccctca acatccatcc tggaggag 720
 gaggatgctg caacattta ctgtcagcac agtagggagc ttccctcggac gttcggtgga 780
 ggcaccaagc tggaaatcaa acgggcggcc gcacccgaagc cttccactcc gcccgggtct 840
 tcccgtatga aacagcttga agacaaaagta gaggagctcc ttagcaagaa ctaccatcta 900
 gaaaacgagg tagctcgct gaaaaagctt gttgggtgaac gtgggtggtaa ccatcaccat 960
 caccattaa 969

<210> 96
 <211> 322
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mAB #8860
 scFv-leucine zipper fusion protein (miniantibody
 vector construct p8860-Zip#1.2)

<400> 96
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15
 Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
 20 25 30

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
 35 40 45
 Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
 50 55 60
 Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
 65 70 75 80
 Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
 85 90 95
 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp
 100 105 110
 Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met
 115 120 125
 Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
 130 135 140
 Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Gln Ile Val Leu
 145 150 155 160
 Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr
 165 170 175
 Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 180 185 190
 Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 195 200 205
 Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
 210 215 220
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu
 225 230 235 240
 Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg
 245 250 255
 Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Pro
 260 265 270
 Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln Leu Glu Asp
 275 280 285
 Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val
 290 295 300
 Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His His His His
 305 310 315 320
 His His

<210> 97
 <211> 270
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:part of plasmid
pMycHis6 differing from vector pCOCK

<400> 97

caggaaacag ctatgaccat gattacgcca agcttccatg aaaattctat ttcaaggaga 60
 cagtcataat gaaataccta ttgcctacgg cagccgctgg attgttatta ctcgcggccc 120
 agccggccat ggcccaggtg cagctgcagg cgccgcctgca ggtcgacctc gagatcaaac 180
 gggcgccgc agaacaaaaa ctcatctcag aagaggatct gaatggggcg gcacatcacc 240
 atcaccatca ctaataagaa ttcaactggcc 270

<210> 98

<211> 61

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:part of plasmid
pMycHis6 differing from vector pCOCK

<400> 98

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Ala Arg Leu Gln Val
 20 25 30

Asp Leu Glu Ile Lys Arg Ala Ala Glu Gln Lys Leu Ile Ser Glu
 35 40 45

Glu Asp Leu Asn Gly Ala Ala His His His His His
 50 55 60

<210> 99

<211> 888

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:198AB2 scFv
linked to c-myc-tag and His6 tag (ORF of
expression vector pMycHis6-198AB2#102)

<220>

<221> modified_base

<222> (228)

<223> n = g, a, c or t

<400> 99

atgaaatacc tattgcctac ggcagccgt ggattgttat tactcgccgc ccagccggcc 60
 atggccgagg tgaagctggg ggagtctggg ggaggcttag tgaagctgg agggtccctg 120
 aaactctcct gtgcagcctc tggattcaact ttcaactgtatc ataccatgtc ttgggttcgc 180
 cagactccgg agaagaggct ggagtgggtc gcaaccattt gtagtggngg tagttccacc 240
 tactatccag acagtgtgaa gggccgatcc accatctcca gagacaatgc caagaacacc 300
 ctgtacctgc aaatgagcag tctgaggtct gaggacacag ccatgttata ctgtacaaga 360
 gaggggggtg gtttaccgtt caactggatc ttcaactgtt ggggcgcagg aacctcagtc 420
 accgtctcct caggtggagg cggttcagggt gggcgccct ctggcggtgg cgatcggac 480
 atttgtgtcga cacagtctcc agcttcttg gctgtgtctc tagggcagag gcccaccata 540
 tcctgcagag ccagtgaaag tggatgtatc attttatgca ctggatcag 600

cagataccag gacagccacc caaactcctc atctatcgtg catccaacct agagtctggg 660
 atccctgcca ggttcagtgg cagtgggtct aggacagact tcaccctcac cattaatcct 720
 gtggaggctg atgatgttgc aaccttattac tgtcagcaaa gtaatgagga tccgctcacg 780
 ttcggtaactg ggaccagact ggaaataaaa cggcgcccg cagaacaaaa actcatctca 840
 gaagaggatc tgaatggggc ggcacatcac catcaccatc actaataa 888

<210> 100
 <211> 294
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:198AB2 scFv
 linked to c-myc-tag and His6 tag (ORF of
 expression vector pMycHis6-198AB2#102)

<400> 100
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15
 Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly
 20 25 30
 Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
 35 40 45
 Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu
 50 55 60
 Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr
 65 70 75 80
 Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
 85 90 95
 Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp
 100 105 110
 Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Phe Thr Val Asn
 115 120 125
 Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser
 130 135 140
 Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Asp
 145 150 155 160
 Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
 165 170 175
 Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly
 180 185 190
 Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
 195 200 205
 Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg
 210 215 220

Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro
 225 230 235 240
 Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu
 245 250 255
 Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala
 260 265 270
 Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
 275 280 285
 His His His His His His
 290

<210> 101
 <211> 876
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mAB #8860 scFv
 linked to c-myc-tag and His6-tag designated
 8860-M/H#4c (plasmid vector p8860-M/H#4c)

<400> 101
 atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc 60
 atggccgagg ttcagcttca gcagtcttga cctgagctgg tgaagcccg ggcctcagtg 120
 aagatttcct gcaaagcttc tggctacgca ttcaagtagct cttggatgaa ctgggtgaag 180
 cagaggcctg gacagggtct tgagtggatt ggacggattt atcctgaaa tgagataact 240
 aactacaatg ggaagttcaa gggcaaggcc acactgactg cagacaaatc ctccagcaca 300
 gcctacatgc agctcagcag cctgacacctt gtgactctg cggcttattt ctgtgcagat 360
 ggtaacgtat attactatgc tatggactac tgggtcaag gaacctcagt caccgtctcc 420
 tcaggtggag gcgggtcagg tgggcgcgccc tctggcggtg gcgatcgca aattgttctc 480
 acccagtctc ctgcttcctt agctgtatct ctggggcaga gggccaccat ctcatgcagg 540
 ggcagcaaaa gtgtcagtagc atctggctat agttatatgc actggtagcca acagaaacca 600
 ggacagccac ccaaactcct catctatctt gcatccaacc tagaatctgg ggtccctgccc 660
 aggttcagtg gcagtggtc tggacagac ttccacctca acatccatcc tggaggag 720
 gaggatgctg caacctatta ctgtcagcac agtagggagc ttccctggac gtcgggtgg 780
 ggcaccaagc tggaaatcaa acggggcgccc gcagaacaaa aactcatctc agaagaggat 840
 ctgaatgggg cggcacatca ccatcaccat cactaa 876

<210> 102
 <211> 291
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mAB #8860 scFv
 linked to c-myc-tag and His6-tag designated
 8860-M/H#4c (plasmid vector p8860-M/H#4c)

<400> 102
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15
 Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
 20 25 30

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
 35 40 45
 Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
 50 55 60
 Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
 65 70 75 80
 Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
 85 90 95
 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp
 100 105 110
 Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met
 115 120 125
 Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
 130 135 140
 Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Gln Ile Val Leu
 145 150 155 160
 Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr
 165 170 175
 Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 180 185 190
 Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 195 200 205
 Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
 210 215 220
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu
 225 230 235 240
 Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg
 245 250 255
 Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu
 260 265 270
 Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala His His His
 275 280 285
 His His His
 290

<210> 103
 <211> 74
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:annealed
 oligonucleotide

<400> 103
 gccccgcagaa caaaaactca tctcagaaga ggatctgaat ggggcggcac atcaccatca 60
 ccatcaactaa taag 74

<210> 104
 <211> 69
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:annealed
 oligonucleotide

<400> 104
 ttatttagtga tggtgatgg t gatgtgcgc cccattcaga tcctcttctg agatgagttt 60
 ttgttctgc 69

<210> 105
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:CDR3 peptide

<220>
 <221> MOD_RES
 <222> (1)..(16)
 <223> Xaa = any amino acid

<400> 105
 Cys Xaa Xaa Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Xaa Xaa Cys
 1 5 10 15

<210> 106
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:CDR3 peptide

<400> 106
 Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp
 1 5 10 15

<210> 107
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:portion of
 plasmid pMycHis6 with pelB-leader, polylinker and
 c-myc tag

<400> 107
Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Ala Arg Leu
1 5 10 15

Gln Val Asp Leu Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys
20 25 30

<210> 108
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:portion of
plasmid pMycHis6 with pelB-leader, polylinker and
c-myc tag

<400> 108
ctcgcggccc agccggccat ggcccaggtg cagctgcagg cgccgcctgca ggtcgaccc 60
gagatcaaac gggcggccgc agaacaaaaa 90

<210> 109
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:c-myc-tag

<400> 109
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly
1 5 10

<210> 110
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:His6-tag

<400> 110
His His His His His
1 5

<210> 111
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:flexible linker

<400> 111
Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser
1 5 10 15

<210> 112

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: A1 peptide core
sequence

<400> 112

Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp

1

5

10